

UID: METH1 - 950aa Type: Protein 950 aa
 METH1 - 950aa (SEQ ID NO:2)
 vs.
 UID: US 6649377 Type: Protein 949 aa
 US 6649377

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Local similarity
    Match: 19
    Mismatch: -17
    Indel start: -13
    Indel extend: -7
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Score: 17959 at (METH1 - 950aa) [2..950] : (US 6649377) [1..949]

2 GNAERAPGSRSFPGVPVPTLLLLAAALLAVSDALGRPSEEEDEELVVPELERAPGHGTTRLRL
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 GNAERAPGSRSFPGVPVPTLLLLAAALLAVSDALGRPSEEEDEELVVPELERAPGHGTTRLRL

62 HAFDQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCIFYSGTVNGDPSSAAA
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
61 HAFDQQLDLELRPDSSFLAPGFTLQNVGRKSGSETPLPETDLAHCIFYSGTVNGDPSSAAA

122 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGCTC
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
121 LSLCEGVRGAFYLLGEAYFIQPLPAASERLATAAPGEKPPAPLQFHLLRRNRQGDVGCTC

182 GVVDDEPRPTGKAETEDEDEGTEGEDEGPQWSPQDPALQGVGQPTGTGSIRKKRFVSSH
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
181 GVVDDEPRPTGKAETEDEDEGTEGEDEGAQWSPQDPALQGVGQPTGTGSIRKKRFVSSH

242 YVETMLVADQSMAEFHGSGLKHYYLTLSVAARLYKHPSIRNSVSLVVKILVIHDEQKG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
241 YVETMLVADQSMAEFHGSGLKHYYLTLSVAARLYKHPSIRNSVSLVVKILVIHDEQKG

302 PEVTSNAALTLRNFCNWQKQHNPSPDRDAEHYDTAILFTRQDLCSQTCDTLGMADVGT
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 PEVTSNAALTLRNFCNWQKQHNPSPDRDAEHYDTAILFTRQDLCSQTCDTLGMADVGT

362 CDPSRSCSVIEDDGLQAFFTAAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
361 CDPSRSCSVIEDDGLQAFFTAAHELGHVFNMPHDDAKQCASLNGVNQDSHMMASMLSNLD

422 HSQPWSPCSAYMITSFLDNHGHECLMDKPQNPIQLPGDLPGTSDANRQCQFTFGEDSKH
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
421 HSQPWSPCSAYMITSFLDNHGHECLMDKPQNPIQLPGDLPGTSDANRQCQFTFGEDSKH

482 CPDAASTCSTLWCTGTSGGVLVCQTKHPWADGTSCGEGKWCINGKCVNKTDRKHFDTPF
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
481 CPDAASTCSTLWCTGTSGGVLVCQTKHPWADGTSCGEGKWCINGKCVNKTDRKHFDTPF

542 HGSWGMWGPWGDCSRTCAGGVQYTMRECDNPVPKNNGKYCEGKRVRYSNCNLEDPCPNNG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
541 HGSWGMWGPWGDCSRTCAGGVQYTMRECDNPVPKNNGKYCEGKRVRYSNCNLEDPCPNNG

602 KTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKVV
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
601 KTFREEQCEAHNEFSKASFGSGPAVEWIPKYAGVSPKDRCKLICQAKGIGYFFVLQPKVV

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662 DGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKISGSVTSAPGY
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
661 DGTPCSPDSTSVCVQGQCVKAGCDRIIDSKKKFDKCGVCGGNGSTCKKISGSVTSAPGY

722 HDIITIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTELSTLEQDIMYKGVV
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
721 HDIITIPTGATNIEVKQRNQRGSRNNGSFLAIKAADGTYILNGDYTELSTLEQDIMYKGVV

782 LRYSGSSAALERIRSFSPLEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAW
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
781 LRYSGSSAALERIRSFSPLEPLTIQVLTVGNALRPKIKYTYFVKKKKESFNAIPTFSAW

842 VIEEWGECSKSCELGWQRRLVECRDINGQPASECAKEVKPASTRPCADHPCPQWQLGEWS
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
841 VIEEWGECSKSCELGWQRRLVECRDINGQPASECAKEVKPASTRPCADHPCPQWQLGEWS

902 SCSKTCGKGYKKRSLKCLSHDGGVLSHESCDPLKKPKHFIDFCTMAECS
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
901 SCSKTCGKGYKKRSLKCLSHDGGVLSHESCDPLKKPKHFIDFCTMAECS

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Percent Identity: 99.7
 Percent Similarity: 99.8

UID: METH2 Type: Protein 890 aa
METH2 (SEQ ID NO:4)
vs.
UID: US 6649377 Type: Protein 949 aa
US 6649377

Local similarity

Match: 19
Mismatch: -17
Indel start: -13
Indel extend: -7

Score: 3038 at (METH2) [20..882] : (US 6649377) [18..880]

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20 LLLPLARGAPARPA---AGGQAS----ELVVP--TRLPGSAG--ELALHLSAF-----GK
   ||| || | | | | | | | | | | | | | | | | | | | | | | | | | |
18 LLL-LA--A-ALLAVSDALGRPSEEEDEELVPELERAPG-HGTTRLRLH--AFDQQLD--

64 GFVLR LAPDDSFLAPEFKIERL---G-GSGRAT-GGERGLRGCFSGTVNGEPESLAAVS
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
68 ---LELRPDSSFLAPGF---TLQNVGRKSGSETPLPETDLAHC FYSGTVNGDPSSAAALS

119 LCRGLSGSF-LLDGE-EFTIQPQGAGGS--L--AQPHRLQRWG---PAGARPL-----
   || | | | | | | | | | | | | | | | | | | | | | | | | | |
123 LCEGVRGAFYLL-GEAYF-IQPLPA-ASERLATAAP-----GEKPPA---PLQFHLLRR

163 PR-----GPEWEV---E---TG--EGQRQERGDHQEDSEEEESQEEEAEGA--SEPP-
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
171 NRQGDVG GTCG---VVDDEPRPTGKAE---TE--D--ED---EGTEGEDEGAQWS--PQ

203 -P-----PLGAT-S-RTKRFVSEARFVETLLVADASMAAFYGADLQNH-ILTLMSVAA
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
215 DPALQGVGQPTG-TGSIRKKRFVSSHRYVETMLVADQSM AEFHGSGL-KHYLLTLFSVAA

253 RIYKHPSIKNSINLMVVKVL-IVEDE-KWGPEV-SDNGGLTLRNFCNWQRRFNQPSDRHP
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
273 RLYKHPSIRNSVSLVVVKILVI-HDEQK-GPEVTS-NAALTLRNFCNWQKQHNPSPDRDA

310 EHYDTAILLTRQNFCG-QEGLCDTLGVADIGTICDPNKSCSVIEDEGLQAAHTLAHELGH
   || | | | | | | | | | | | | | | | | | | | | | | | | | |
330 EHYDTAILFTRQDLCSQ--TCDTLGMADVGTVC DPSRSCSVIEDDGLQAAFTTAHELGH

369 VLSMPHDDSKPCTRLFGPMGKHHV-----MA-PLFVHLN----QTLPWSPCSA-MYLTE
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
388 VFNMPHDDAKQCASLNG-----VNQDSHMMASML---SNLDHSQ--PWSPCSAYM-ITS

417 LLDGGHGDCLLDAPGAALP--LPTG-LPGRMALYQLD--QQCRQ-IFGPDFRHC PNTSAQ
   || | | | | | | | | | | | | | | | | | | | | | | | | | |
436 FLDNGHGECLMDKP--QNPIQLP-GDLPG--TSY--DANRQC-QFTFGEDSKHCP-----

471 D---VCAQLWC-HTDGAEPL-CHTKNGSLPWADGTPCGPGHLCSEGSCLP EEEV---ERP
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
483 DAASTCSTLWCTGTSG-GVLVCQTK--HFPWADGTSCGEGKWCINGKC-----VNKTHR-

523 K----PVVDGGWAPWGPWGECSRTCGGGVQF SHRECKD-PEPQNGGRYCLG-R-RAKYQS
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
534 KHFDTP-FHGSWGMWGPWGDCSRTCGGGVQYTMREC-DNPVPKNGGKYCEGKRVR--YRS
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